

1653

RAW SEQUENCE LISTING

DATE: 08/15/2001

PATENT APPLICATION: US/09/518,297

TIME: 12:28:02

Input Set : A:\4600-0130.30-SEQLIST.TXT

Output Set: N:\CRF3\08152001\I518297.raw

ENTERED

4 <110> APPLICANT: Lim, Moon Young
 5 Edwards, Cynthia A.
 6 Fry, Kirk E.
 7 Bruice, Thomas W.
 8 Starr, Douglas B.
 9 Laurance, Megan E.
 10 Kwok, Yan
 13 <120> TITLE OF INVENTION: DNA Binding Compound-Mediated Molecular
 14 Switch System
 16 <130> FILE REFERENCE: 4600-0130.30
 18 <140> CURRENT APPLICATION NUMBER: US 09/518,297
 19 <141> CURRENT FILING DATE: 2000-03-03
 21 <150> PRIOR APPLICATION NUMBER: US 60/122,513
 22 <151> PRIOR FILING DATE: 1999-03-03
 24 <150> PRIOR APPLICATION NUMBER: US 60/154,605
 25 <151> PRIOR FILING DATE: 1999-09-17
 27 <160> NUMBER OF SEQ ID NOS: 62
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 11
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: DNA response element
 39 <400> SEQUENCE: 1
 40 cggttcgcact t 11
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 17
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Artificial Sequence
 47 <220> FEATURE:
 48 <223> OTHER INFORMATION: DNA response element
 50 <400> SEQUENCE: 2
 51 cggagtactg tcctccg 17
 53 <210> SEQ ID NO: 3
 54 <211> LENGTH: 12
 55 <212> TYPE: DNA
 56 <213> ORGANISM: Artificial Sequence
 58 <220> FEATURE:
 59 <223> OTHER INFORMATION: DNA response element
 61 <221> NAME/KEY: misc_feature
 62 <222> LOCATION: (1)...(12)
 63 <223> OTHER INFORMATION: n = A,T,C or G
 65 <400> SEQUENCE: 3
 66 taattanggg ng 12
 68 <210> SEQ ID NO: 4
 69 <211> LENGTH: 551

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70 <212> TYPE: PRT
71 <213> ORGANISM: Homo sapiens
73 <220> FEATURE:
74 <221> NAME/KEY: VARIANT
75 <222> LOCATION: (0)...(0)
76 <223> OTHER INFORMATION: transcriptional regulatory protein
78 <400> SEQUENCE: 4
79 Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala
80 1 5 10 15
81 Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
82 20 25 30
83 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
84 35 40 45
85 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
86 50 55 60
87 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
88 65 70 75 80
89 Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
90 85 90 95
91 Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
92 100 105 110
93 Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
94 115 120 125
95 Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
96 130 135 140
97 Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
98 145 150 155 160
99 Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
100 165 170 175
101 Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
102 180 185 190
103 Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
104 195 200 205
105 Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
106 210 215 220
107 Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
108 225 230 235 240
109 Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
110 245 250 255
111 Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu
112 260 265 270
113 Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr
114 275 280 285
115 Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg
116 290 295 300
117 Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly
118 305 310 315 320
119 Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg
120 325 330 335

```

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```

121 Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr
122          340          345          350
123 Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe
124          355          360          365
125 Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro
126          370          375          380
127 Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val
128 385          390          395          400
129 Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly
130          405          410          415
131 Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
132          420          425          430
133 Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
134          435          440          445
135 Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
136          450          455          460
137 Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
138 465          470          475          480
139 Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
140          485          490          495
141 Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
142          500          505          510
143 Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
144          515          520          525
145 Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
146          530          535          540
147 Leu Leu Ser Gln Ile Ser Ser
148 545          550

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150 <210> SEQ ID NO: 5

151 <211> LENGTH: 19

152 <212> TYPE: DNA

153 <213> ORGANISM: Artificial Sequence

155 <220> FEATURE:

156 <223> OTHER INFORMATION: DNA response element

158 <400> SEQUENCE: 5

159 tccctatcag tgatagaga

19

161 <210> SEQ ID NO: 6

162 <211> LENGTH: 22

163 <212> TYPE: DNA

164 <213> ORGANISM: Artificial Sequence

166 <220> FEATURE:

167 <223> OTHER INFORMATION: response element

169 <400> SEQUENCE: 6

170 cttaacactc gcgagtgtta ag

22

172 <210> SEQ ID NO: 7

173 <211> LENGTH: 13

174 <212> TYPE: DNA

175 <213> ORGANISM: Artificial Sequence

177 <220> FEATURE:

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178 <223> OTHER INFORMATION: response element

180 <221> NAME/KEY: misc_feature

181 <222> LOCATION: (3)...(3)

182 <223> OTHER INFORMATION: n = G or T

184 <221> NAME/KEY: misc_feature

185 <222> LOCATION: (7)...(7)

186 <223> OTHER INFORMATION: n = A,T,C or G

188 <221> NAME/KEY: misc_feature

189 <222> LOCATION: (12)...(12)

190 <223> OTHER INFORMATION: n = A or C

192 <400> SEQUENCE: 7

193 rgntcantga cny

13

195 <210> SEQ ID NO: 8

196 <211> LENGTH: 77

197 <212> TYPE: PRT

198 <213> ORGANISM: Artificial Sequence

200 <220> FEATURE:

201 <223> OTHER INFORMATION: activator sequence

203 <400> SEQUENCE: 8

204 Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly

205 1 5 10 15

206 Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu

207 20 25 30

208 Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His

209 35 40 45

210 Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu

211 50 55 60

212 Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly

213 65 70 75

215 <210> SEQ ID NO: 9

216 <211> LENGTH: 11

217 <212> TYPE: PRT

218 <213> ORGANISM: Artificial Sequence

220 <220> FEATURE:

221 <223> OTHER INFORMATION: activator sequence

223 <221> NAME/KEY: VARIANT

224 <222> LOCATION: (1)...(11)

225 <223> OTHER INFORMATION: tetramer

227 <400> SEQUENCE: 9

228 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu

229 1 5 10

231 <210> SEQ ID NO: 10

232 <211> LENGTH: 97

233 <212> TYPE: PRT

234 <213> ORGANISM: Artificial Sequence

236 <220> FEATURE:

237 <223> OTHER INFORMATION: repressor sequence

239 <400> SEQUENCE: 10

240 Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe

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Input Set : A:\4600-0130.30-SEQLIST.TXT

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```

241 1           5           10           15
242 Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
243           20           25           30
244 Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
245           35           40           45
246 Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
247           50           55           60
248 Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
249 65           70           75           80
250 Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
251           85           90           95
252 Val
255 <210> SEQ ID NO: 11
256 <211> LENGTH: 36
257 <212> TYPE: PRT
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: repressor sequence
263 <400> SEQUENCE: 11
264 Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
265 1           5           10           15
266 Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
267           20           25           30
268 Met Leu Pro Tyr
269           35
271 <210> SEQ ID NO: 12
272 <211> LENGTH: 116
273 <212> TYPE: DNA
274 <213> ORGANISM: Escherichia coli
276 <220> FEATURE:
277 <221> NAME/KEY: misc_feature
278 <222> LOCATION: (0)...(0)
279 <223> OTHER INFORMATION: partial promoter sequence
281 <400> SEQUENCE: 12
282 cgcggtcaga aaattatattt aaatttcctc ttgtcaggcc ggaataactc cctataatgc      60
283 gccaccactg acacggaaca acggcaaaca cgccgccggg tcagcggggt tctcct      116
285 <210> SEQ ID NO: 13
286 <211> LENGTH: 22
287 <212> TYPE: DNA
288 <213> ORGANISM: Escherichia coli
290 <220> FEATURE:
291 <221> NAME/KEY: misc_feature
292 <222> LOCATION: (0)...(0)
293 <223> OTHER INFORMATION: partial promoter sequence
295 <400> SEQUENCE: 13
296 agaaaattat tttaaatttc ct      22
298 <210> SEQ ID NO: 14
299 <211> LENGTH: 22
300 <212> TYPE: DNA

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/518,297

DATE: 08/15/2001

TIME: 12:28:03

Input Set : A:\4600-0130.30-SEQLIST.TXT

Output Set: N:\CRF3\08152001\I518297.raw

L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7